

1646

RAW SEQUENCE LISTING DATE: 09/26/2000
PATENT APPLICATION: US/09/662,783 TIME: 11:55:50

Input Set : A:\Cura-77.app
Output Set: N:\CRF3\09262000\I662783.raw

3 <110> APPLICANT: Lichenstein, Henri
4 Shimkets, Richard A.
5 Herrmann, John
6 Boldog, Ferenc
8 <120> TITLE OF INVENTION: Growth Factor Polypeptides and Nucleic Acids Encoding
9 Same
11 <130> FILE REFERENCE: 15966-577 (Cura-77)
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/662,783
14 <141> CURRENT FILING DATE: 2000-09-12
16 <150> PRIOR APPLICATION NUMBER: USSN 60/158,083
17 <151> PRIOR FILING DATE: 1999-10-07
19 <150> PRIOR APPLICATION NUMBER: USSN 60/186,707
20 <151> PRIOR FILING DATE: 2000-03-03
22 <150> PRIOR APPLICATION NUMBER: USSN 60/188,250
23 <151> PRIOR FILING DATE: 2000-03-10
25 <150> PRIOR APPLICATION NUMBER: USSN 60/159,231
26 <151> PRIOR FILING DATE: 1999-10-13
28 <150> PRIOR APPLICATION NUMBER: USSN 60/174,485
29 <151> PRIOR FILING DATE: 2000-01-04
31 <150> PRIOR APPLICATION NUMBER: USSN 60/223,879
32 <151> PRIOR FILING DATE: 2000-08-08
34 <160> NUMBER OF SEQ ID NOS: 24
36 <170> SOFTWARE: PatentIn Ver. 2.0
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40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
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44 <221> NAME/KEY: CDS
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52 gtcggcgag cagaaccccg cttttcttg gagcgacgct gctctctg 180
54 a atg cac cgg ctc atc ttt gtc tac act cta atc tgc gca aac ttt tgc 229
55 Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
56 1 5 10 15
58 agc tgt cgg gac act tct gca acc ccg cag agc gca tcc aaa gct 277
59 Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
60 20 25 30
62 ttg cgc aac gcc aac ctc agg cga gat gag agc aat cac ctc aca gac 325
63 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
64 35 40 45
66 ttg tac cga aga gat gag acc atc cag gtg aaa gga aac ggc tac gtg 373
67 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
68 50 55 60
70 cag agt cct aga ttc ccg aac agc tac ccc agg aac ctg ctc cta aca 421

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72	65					70					75				80	
74	tgg	cgg	ctt	cac	tct	cag	gag	aat	aca	cgg	ata	cag	cta	gtg	ttt	gac
75	Trp	Arg	Leu	His	Ser	Gln	Glu	Asn	Thr	Arg	Ile	Gln	Leu	Val	Phe	Asp
76						85					90			95		469
78	aat	cag	ttt	gga	tta	gag	gaa	gca	gaa	aat	gat	atc	tgt	agg	tat	gat
79	Asn	Gln	Phe	Gly	Leu	Glu	Glu	Ala	Glu	Asn	Asp	Ile	Cys	Arg	Tyr	Asp
80						100				105			110			517
82	ttt	gtg	gaa	gtt	gaa	gat	ata	tcc	gaa	acc	agt	acc	att	att	aga	gga
83	Phe	Val	Glu	Val	Glu	Asp	Ile	Ser	Glu	Thr	Ser	Thr	Ile	Ile	Arg	Gly
84						115				120			125			565
86	cga	tgg	tgt	gga	cac	aag	gaa	gtt	cct	cca	agg	ata	aaa	tca	aga	acg
87	Arg	Trp	Cys	Gly	His	Lys	Glu	Val	Pro	Pro	Arg	Ile	Lys	Ser	Arg	Thr
88						130				135			140			613
90	aac	caa	att	aaa	atc	aca	ttc	aag	tcc	gat	gac	tac	ttt	gtg	gct	aaa
91	Asn	Gln	Ile	Lys	Ile	Thr	Phe	Lys	Ser	Asp	Asp	Tyr	Phe	Val	Ala	Lys
92	145					150				155			160			
94	cct	gga	ttc	aag	att	tat	tat	tct	ttg	ctg	gaa	gat	ttc	caa	ccc	gca
95	Pro	Gly	Phe	Lys	Ile	Tyr	Tyr	Ser	Leu	Leu	Glu	Asp	Phe	Gln	Pro	Ala
96						165				170			175			709
98	gca	gtc	tca	gag	acc	aac	tgg	gaa	tct	gtc	aca	agc	tct	att	tca	ggg
99	Ala	Ala	Ser	Glu	Thr	Asn	Trp	Glu	Ser	Val	Thr	Ser	Ser	Ile	Ser	Gly
100						180				185			190			757
102	gta	tcc	tat	aac	tct	cca	tca	gta	acg	gat	ccc	act	ctg	att	gcg	gat
103	Val	Ser	Tyr	Asn	Ser	Pro	Ser	Val	Thr	Asp	Pro	Thr	Leu	Ile	Ala	Asp
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106	gct	ctg	gac	aaa	aaa	att	gca	gaa	ttt	gat	aca	gtg	gaa	gat	ctg	ctc
107	Ala	Leu	Asp	Lys	Lys	Ile	Ala	Glu	Phe	Asp	Thr	Val	Glu	Asp	Leu	Leu
108						210				215			220			853
110	aag	tac	tcc	aat	cca	gag	tca	tgg	caa	gaa	gat	ctt	gag	aat	atg	tat
111	Lys	Tyr	Phe	Asn	Pro	Glu	Ser	Trp	Gln	Glu	Asp	Leu	Glu	Asn	Met	Tyr
112	225					230				235			240			901
114	ctg	gac	acc	cct	cg	tat	cga	ggc	agg	tca	tac	cat	gac	cg	aag	tca
115	Leu	Asp	Thr	Pro	Arg	Tyr	Arg	Gly	Arg	Ser	Tyr	His	Asp	Arg	Lys	Ser
116						245				250			255			949
118	aaa	gtt	gac	ctg	gat	agg	ctc	aat	gat	gtc	aaa	cgt	tac	agt	tgc	
119	Lys	Val	Asp	Leu	Asp	Arg	Leu	Asn	Asp	Asp	Ala	Lys	Arg	Tyr	Ser	Cys
120						260				265			270			1045
122	act	ccc	agg	aat	tac	tcg	gtc	aat	ata	aga	gaa	gag	ctg	aag	ttg	gcc
123	Thr	Pro	Arg	Asn	Tyr	Ser	Val	Asn	Ile	Arg	Glu	Glu	Leu	Lys	Leu	Ala
124						275				280			285			1093
126	aat	gtg	gtc	ttc	ttt	cca	cgt	tgc	ctc	gtc	cag	cgc	tgt	gg	gg	
127	Asn	Val	Val	Phe	Phe	Pro	Arg	Cys	Leu	Leu	Val	Gln	Arg	Cys	Gly	Gly
128						290				295			300			1141
130	aat	tgt	ggc	tgt	gga	act	gtc	aac	tgg	agg	tcc	tgc	aca	tgc	aat	tca
131	Asn	Cys	Gly	Cys	Gly	Thr	Val	Asn	Trp	Arg	Ser	Cys	Thr	Cys	Asn	Ser
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134	ggg	aaa	acc	gtg	aaa	aag	tat	cat	gag	gt	tta	cag	ttt	gag	cct	ggc
135	Gly	Lys	Thr	Val	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Phe	Glu	Pro	Gly

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138 cac atc aag agg agg ggt aga gct aag acc atg gct cta gtt gac atc 1237
139 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
140          340          345          350
142 cag ttg gat cac cat gaa cga tgt gat tgt atc tgc agc tca aga cca 1285
143 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
144          355          360          365
146 cct cga taagagaatg tgcacatcct tacattaagc ctgaaagaac ctttagttta 1341
147 Pro Arg
148          370
150 aggagggtga gataagagac cctttccta ccagcaacca aacttactac tagccgtcaa 1401
152 tgcaatgaac acaagtggtt gctgagtc tgccttgcgtt tgtaatgcc atggcaagta 1461
154 gaaagggtata tcatcaactt cttacactaa gaatataatgg ttgcatttaa taatagttt 1521
156 tgaggttata tatgcacaaa cacacacaga aatataatca tgcctatgtt tataatagatc 1581
158 aaatgttttt ttgttatata ataaccaggc acaccaggc ttacataatgtt tgagttaga 1641
160 ctcttaaat ccttgccaa aataagggtt ggtcaatata atgaaacatgt tcttttagaaa 1701
162 attttaggaga taaaattttt tttttttt gaaacacaaa acaattttga atcttgctct 1761
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179          20          25          30
181 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
182          35          40          45
184 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
185          50          55          60
187 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
188          65          70          75          80
190 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
191          85          90          95
193 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
194          100          105          110
196 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
197          115          120          125
199 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
200          130          135          140
202 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
203          145          150          155          160
205 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
206          165          170          175
208 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
209          180          185          190
211 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp

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212 195 200 205
 214 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 215 210 215 220
 217 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
 218 225 230 235 240
 220 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 221 245 250 255
 223 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
 224 260 265 270
 226 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
 227 275 280 285
 229 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 230 290 295 300
 232 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
 233 305 310 315 320
 235 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
 236 325 330 335
 238 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
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 241 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
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 262 ttggattaga ggaagcagaa aatgatatct gtaggtatga ttttggaa gttgaagata 180
 264 tatccaaac cagtaccatt atttagggac gatgggtgaa acacaaggaa gttccctcaa 240
 266 ggataaaaatc aagaacgaac caaattaaaa tcacattcaa gtccgatgac tactttgtgg 300
 268 ctaaacatgg attcaagatt tattattctt tgctggaa ttccaaaccc gcagcagctt 360
 270 cagagaccaa ctggaaatct gtccacaagct ctatccagg ggtatccat aactctccat 420
 272 cagtaacgga tccactctg attccggatg ctctggacaa aaaatttgcg gaatttgata 480
 274 cagtggaga tctgctcaag tacttcaatc cagagtcatg gcaagaagat cttgagaat 539
 276 atg tat ctg gac acc cct cgg tat cga ggc agg tca tac cat gac cgg 587
 277 Met Tyr Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg
 278 1 5 10 15
 280 aag tca aaa gtt gac ctg gat agg ctc aat gat gat gat gcc aag cgt tac 635
 281 Lys Ser Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr
 282 20 25 30
 284 agt tgc act ccc agg aat tac tcg gtc aat ata aga gaa gag ctg aag 683
 285 Ser Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys
 286 35 40 45

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289 Leu Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys
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292 gga gga aat tgt ggc tgt gga act gtc aac tgg agg tcc tgc aca tgc 779
293 Gly Gly Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys
294 65 70 75 80
296 aat tca ggg aaa acc gtg aaa aag tat cat gag gta tta cag ttt gag 827
297 Asn Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu
298 85 90 95
300 cct ggc cac atc aag agg agg ggt aga gct aag acc atg gct cta gtt 875
301 Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val
302 100 105 110
304 gac atc cag ttg gat cac cat gaa cga tgt gat tgt atc tgc agc tca 923
305 Asp Ile Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser
306 115 120 125
308 aga cca cct cga taagagaatg tgcacatct tacattaagc ctgaaagaac 975
309 Arg Pro Pro Arg
310 130
312 cttagttta aggagggtga gataagagac cctttccta ccagcaacca aacttactac 1035
314 tagcctgcaa tgcataaac acaagtgggt gctgagtc acgccttgctt tgtaatgcc 1095
316 atggcaagta gaaaggata tcatcaactt ctatacataa gaataataggta ttgcatttaa 1155
318 taatagtgtt tgaggttata tatgcacaaa cacacacaga aataatattca tgcctatgt 1215
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322 ttgagttaga ctcttaaaat ccttgccaa aataaggat ggtcaatataatgaaacatg 1335
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326 atcttgctct cttaaagaaa gcacatgtta tattaaaaat caaaatgtga ggctttctta 1455
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336 <211> LENGTH: 132
337 <212> TYPE: PRT
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348 35 40 45
350 Leu Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys
351 50 55 60
353 Gly Gly Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys
354 65 70 75 80
356 Asn Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu
357 85 90 95
359 Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val
360 100 105 110
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/662,783

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number